

RAW SEQUENCE LISTING

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Application Serial Number: 10/555,544
Source: JFWP
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/555,544

DATE: 11/01/2006

TIME: 11:06:12

Input Set : A:\SAEG129.016APCSequence Listing.txt

Output Set: N:\CRF4\11012006\J555544.raw

3 <110> APPLICANT: Ohmiya, Yoshihiro
 4 Nakajima, Yoshihiro
 6 <120> TITLE OF INVENTION: Multiple gene transcription activity assay system
 8 <130> FILE REFERENCE: SAEG129.016APC
 10 <140> CURRENT APPLICATION NUMBER: 10/555,544
 C--> 11 <141> CURRENT FILING DATE: 2005-11-04
 13 <150> PRIOR APPLICATION NUMBER: JP2003-127629
 14 <151> PRIOR FILING DATE: 2003-05-06
 16 <150> PRIOR APPLICATION NUMBER: JP2003-407564
 17 <151> PRIOR FILING DATE: 2003-12-05
 19 <160> NUMBER OF SEQ ID NOS: 65
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1638
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Wild Type Phrixothrix Green Luciferase
 28 <400> SEQUENCE: 1
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 31 gcaggacaac aattataccat atcattgtat aaatttgcattt ctttcctga agcaataatc 120
 33 gatgctcata caaatgaagt aatatcatat gctcaaatat ttgaaaccag ctgcgcgtta 180
 35 gctgttagta tagaacaata tggcttgaat gaaaacaatg ttgtgggtgt atgcagtgaa 240
 37 aacaatataa actttttaa tcctgtcctt gctgcattat acttaggaat accagtagca 300
 39 acatcaaatg atatgtacac agatggagag ttaactggtc atttgaatat atcaaaacca 360
 41 actatcatgt tttagttcaaa gaaagcactc ccgcatttgc tgagagtaca gcaaaatcta 420
 43 agtttcatta aaaaagtgcgt agttatcgat agcatgtacg acattaaatgg cggttgaatgc 480
 45 gtatctaccc ttgttgcacg ttatactgac cacaccccttgc atccattgtc atttacacca 540
 47 aaagatttttgc aaaaatcgca ttaattatgt catcatctgg aacaactgg 600
 49 ttgccttaagg gtgttagtact gagccataga agtctaacta taagattcgt tcatacgagg 660
 51 gatcccattt atggcaactcg tacgggttcca caaacatcaa ttctttccctt agtaccgttc 720
 53 catcatgcct ttggaatgtt tactacatta tcttactttg tagtaggact taagttgtta 780
 55 atgttgaaga aatttgaggg cgcaacttttgc ttaaaaaacca tacagaattta caaaatcccc 840
 57 actattgttag tggccctcc agttatgggt tttttggctta aagccccatt agtgcattca 900
 59 tacgattttat cgagcttaac ggaagttgcgt actggaggag ctccttttagg aaaagatgtc 960
 61 gcagaagcag tagcaaagag gttgaaatata cctgaaatca tacaaggata tggattaaact 1020
 63 gaaacttgct ggcgttaat gattacccct cataatgtcg tgaaaaacagg ttcaactgg 1080
 65 agacccttgc catacattaa agctaaatgtt tagataacg ctactggaa ggcgttagga 1140
 67 ccaggagaaa gaggcgaaat atgctttaaa agtggaaatgatgaaatgg atattacaac 1200
 69 aatccggaaag caactattga tactattgac aaagatgggt ggcttcattc tggagatatt 1260
 71 ggatattacg acgaagatgg aaatttcttt atagttgatc gattgaaaga acttattaaa 1320
 73 tacaaggat atcaggttgc gctgctgaa ctggaaaatc tgctttaca acatccaatgt 1380
 75 attgctgatg cgggtttac tggagttccg gacgaaatgg ctggacaattt acctgctgct 1440
 77 tgtgttgtgt tagaatctgg caagacgctg actgaaaagg aagttcaaga ttttattgca 1500
 79 gcacaagtca ctccaaacaaa gcatcttcga ggccgtgtcg tattttaga cagtattccg 1560

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83 cccaaaatcaa aattataa 1638
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87 <211> LENGTH: 545
88 <212> TYPE: PRT
89 <213> ORGANISM: Wild Type Phrixothrix Green Luciferase
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94 1 5 10 15
97 His Pro Gly Ser Ala Gly Gln Gln Leu Tyr Gln Ser Leu Tyr Lys Phe
98 20 25 30
101 Ala Ser Phe Pro Glu Ala Ile Ile Asp Ala His Thr Asn Glu Val Ile
102 35 40 45
105 Ser Tyr Ala Gln Ile Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Ile
106 50 55 60
109 Glu Gln Tyr Gly Leu Asn Glu Asn Asn Val Val Gly Val Cys Ser Glu
110 65 70 75 80
113 Asn Asn Ile Asn Phe Phe Asn Pro Val Leu Ala Ala Leu Tyr Leu Gly
114 85 90 95
117 Ile Pro Val Ala Thr Ser Asn Asp Met Tyr Thr Asp Gly Glu Leu Thr
118 100 105 110
121 Gly His Leu Asn Ile Ser Lys Pro Thr Ile Met Phe Ser Ser Lys Lys
122 115 120 125
125 Ala Leu Pro Leu Ile Leu Arg Val Gln Gln Asn Leu Ser Phe Ile Lys
126 130 135 140
129 Lys Val Val Val Ile Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys
130 145 150 155 160
133 Val Ser Thr Phe Val Ala Arg Tyr Thr Asp His Thr Phe Asp Pro Leu
134 165 170 175
137 Ser Phe Thr Pro Lys Asp Phe Asp Pro Leu Glu Lys Ile Ala Leu Ile
138 180 185 190
141 Met Ser Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Val Leu Ser
142 195 200 205
145 His Arg Ser Leu Thr Ile Arg Phe Val His Ser Arg Asp Pro Ile Tyr
146 210 215 220
149 Gly Thr Arg Thr Val Pro Gln Thr Ser Ile Leu Ser Leu Val Pro Phe
150 225 230 235 240
153 His His Ala Phe Gly Met Phe Thr Thr Leu Ser Tyr Phe Val Val Gly
154 245 250 255
157 Leu Lys Val Val Met Leu Lys Lys Phe Glu Gly Ala Leu Phe Leu Lys
158 260 265 270
161 Thr Ile Gln Asn Tyr Lys Ile Pro Thr Ile Val Val Ala Pro Pro Val
162 275 280 285
165 Met Val Phe Leu Ala Lys Ser Pro Leu Val Asp Gln Tyr Asp Leu Ser
166 290 295 300
169 Ser Leu Thr Glu Val Ala Thr Gly Gly Ala Pro Leu Gly Lys Asp Val
170 305 310 315 320
173 Ala Glu Ala Val Ala Lys Arg Leu Lys Leu Pro Gly Ile Ile Gln Gly
174 325 330 335

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177 Tyr Gly Leu Thr Glu Thr Cys Cys Ala Val Met Ile Thr Pro His Asn
 178 340 345 350
 181 Ala Val Lys Thr Gly Ser Thr Gly Arg Pro Leu Pro Tyr Ile Lys Ala
 182 355 360 365
 185 Lys Val Leu Asp Asn Ala Thr Gly Lys Ala Leu Gly Pro Gly Glu Arg
 186 370 375 380
 189 Gly Glu Ile Cys Phe Lys Ser Glu Met Ile Met Lys Gly Tyr Tyr Asn
 190 385 390 395 400
 193 Asn Pro Glu Ala Thr Ile Asp Thr Ile Asp Lys Asp Gly Trp Leu His
 194 405 410 415
 197 Ser Gly Asp Ile Gly Tyr Tyr Asp Glu Asp Gly Asn Phe Phe Ile Val
 198 420 425 430
 201 Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro
 202 435 440 445
 205 Ala Glu Leu Glu Asn Leu Leu Gln His Pro Ser Ile Ala Asp Ala
 206 450 455 460
 209 Gly Val Thr Gly Val Pro Asp Glu Phe Ala Gly Gln Leu Pro Ala Ala
 210 465 470 475 480
 213 Cys Val Val Leu Glu Ser Gly Lys Thr Leu Thr Glu Lys Glu Val Gln
 214 485 490 495
 217 Asp Phe Ile Ala Ala Gln Val Thr Pro Thr Lys His Leu Arg Gly Gly
 218 500 505 510
 221 Val Val Phe Val Asp Ser Ile Pro Lys Gly Pro Thr Gly Lys Leu Ile
 222 515 520 525
 225 Arg Lys Glu Leu Arg Glu Ile Phe Ala Gln Arg Ala Pro Lys Ser Lys
 226 530 535 540
 229 Leu
 230 545
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 234 <211> LENGTH: 1641
 235 <212> TYPE: DNA
 236 <213> ORGANISM: Wild Type Phrixothrix Red Luciferase
 238 <400> SEQUENCE: 3
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 241 gcaggactac aattatatca atcattatataa aatattcat atattactga cgaaataatc 120
 243 gatgccata ccaatgaagt aatatcatat gctcaaataat ttgaaaccag ctggcgcttg 180
 245 gcagttagtc tagaaaaata tggcttgat cataacaatg ttgtggcaat atgcagtggaa 240
 247 aacaacatac actttttgg ccctttaatt gctgcttat accaaggaaat accaatggca 300
 249 acatcaaatg atatgtacac agaaaggag atgattggcc atttgaatat atcgaaaccca 360
 251 tgccttatgt tttgttcaaa gaaatcactc ccatttatic tgaaagtaca aaaacatcta 420
 253 gatttcctta aaaaagtcat agtcattgtat agtatgtacg atatcaatgg cgttgaatgc 480
 255 gtatttagct ttgtttcacg ttatactgtat cacgccttgc atccagtggaa atttaaccca 540
 257 aaagagttt atcccttggaa aagaaccgca ttaattatga catcatctgg aacaactggaa 600
 259 ttgcctaaag gggtagtaat aagccataga agtataacta taagattcgatccatagcagt 660
 261 gatcccatct atggtaactcg tattgctcca gatacatcaa ttcttgctat agcaccgttc 720
 263 catcatgcct ttggactgtt tactgcacta gcttactttc cagtaggact taagattgtat 780
 265 atggtaaga aatttgaggcgaaattcttc ttaaaaacca tacaaaaatcaaaatcgct 840
 267 tctattgtat ttcccttc aattatggta tattggcta aaagtccatt agtcgatgaa 900
 269 tacaatttat cgagcttaac ggaaattgct tggagggtt ctcctttagg aagagatatc 960

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271	gcagataaaag	tagcaaagag	attgaaaagta	catggaatcc	tacaaggata	tggattaacc	1020										
273	gaaaacctgca	gcgctcta	acttagcccc	aatgatcgag	aacttaaaaa	aggtaatt	1080										
275	ggaaacgccta	tgccatata	gtcaagttaa	gttata	gata	tcaataactgg	1140										
277	ggaccaagag	aaaaaggcga	aatatgctc	aaaagtcaaa	tgcttatgaa	aggatatcac	1200										
279	aacaatccgc	aagcaactcg	tgatgctctt	gacaaagatg	gttggctca	tactggggat	1260										
281	cttggatatt	acgacgaaga	cagatttac	tatgtatgg	atcgattgaa	agaacttatt	1320										
283	aatatataaaag	gatatcagg	tgccgctgt	gaactggaaa	atctgcttt	acaacatcca	1380										
285	aatatattctg	atgcgggtgt	tattggatt	ccggacgaat	ttgctggta	attaccttcc	1440										
287	gcgtgtgttg	tgttagagcc	ttgtaagaca	atgaccgaaa	aggaagtca	ggattatatt	1500										
289	gcagagctag	tcactacaac	taaacatctt	cgaggcggtg	tcgtatttat	agatagtatt	1560										
291	ccaaaaggcc	caacaggaaa	actcatgaga	aacgaactcc	gtgcaatatt	tgcccccggaa	1620										
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308					20				25					30			
311	Ser	Tyr	Ile	Thr	Asp	Gly	Ile	Ile	Asp	Ala	His	Thr	Asn	Glu	Val	Ile	
312					35				40					45			
315	Ser	Tyr	Ala	Gln	Ile	Phe	Glu	Thr	Ser	Cys	Arg	Leu	Ala	Val	Ser	Leu	
316					50				55					60			
319	Glu	Lys	Tyr	Gly	Leu	Asp	His	Asn	Asn	Val	Val	Ala	Ile	Cys	Ser	Glu	
320					65				70					75		80	
323	Asn	Asn	Ile	His	Phe	Phe	Gly	Pro	Leu	Ile	Ala	Ala	Leu	Tyr	Gln	Gly	
324					85				90					95			
327	Ile	Pro	Met	Ala	Thr	Ser	Asn	Asp	Met	Tyr	Thr	Glu	Arg	Glu	Met	Ile	
328					100				105					110			
331	Gly	His	Leu	Asn	Ile	Ser	Lys	Pro	Cys	Leu	Met	Phe	Cys	Ser	Lys	Lys	
332					115				120					125			
335	Ser	Leu	Pro	Phe	Ile	Leu	Lys	Val	Gln	Lys	His	Leu	Asp	Phe	Leu	Lys	
336					130				135					140			
339	Lys	Val	Ile	Val	Ile	Asp	Ser	Met	Tyr	Asp	Ile	Asn	Gly	Val	Glu	Cys	
340					145				150					155		160	
343	Val	Phe	Ser	Phe	Val	Ser	Arg	Tyr	Thr	Asp	His	Ala	Phe	Asp	Pro	Val	
344					165				170					175			
347	Lys	Phe	Asn	Pro	Lys	Glu	Phe	Asp	Pro	Leu	Glu	Arg	Thr	Ala	Leu	Ile	
348					180				185					190			
351	Met	Thr	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Val	Ile	Ser	
352					195				200					205			
355	His	Arg	Ser	Ile	Thr	Ile	Arg	Phe	Val	His	Ser	Ser	Asp	Pro	Ile	Tyr	
356					210				215					220			
359	Gly	Thr	Arg	Ile	Ala	Pro	Asp	Thr	Ser	Ile	Leu	Ala	Ile	Ala	Pro	Phe	
360					225				230					235		240	
363	His	His	Ala	Phe	Gly	Leu	Phe	Thr	Ala	Leu	Ala	Tyr	Phe	Pro	Val	Gly	
364					245				250					255			

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367 Leu Lys Ile Val Met Val Lys Lys Phe Glu Gly Glu Phe Phe Leu Lys
 368 260 265 270
 371 Thr Ile Gln Asn Tyr Lys Ile Ala Ser Ile Val Val Pro Pro Pro Ile
 372 275 280 285
 375 Met Val Tyr Leu Ala Lys Ser Pro Leu Val Asp Glu Tyr Asn Leu Ser
 376 290 295 300
 379 Ser Leu Thr Glu Ile Ala Cys Gly Gly Ser Pro Leu Gly Arg Asp Ile
 380 305 310 315 320
 383 Ala Asp Lys Val Ala Lys Arg Leu Lys Val His Gly Ile Leu Gln Gly
 384 325 330 335
 387 Tyr Gly Leu Thr Glu Thr Cys Ser Ala Leu Ile Leu Ser Pro Asn Asp
 388 340 345 350
 391 Arg Glu Leu Lys Lys Gly Ala Ile Gly Thr Pro Met Pro Tyr Val Gln
 392 355 360 365
 395 Val Lys Val Ile Asp Ile Asn Thr Gly Lys Ala Leu Gly Pro Arg Glu
 396 370 375 380
 399 Lys Gly Glu Ile Cys Phe Lys Ser Gln Met Leu Met Lys Gly Tyr His
 400 385 390 395 400
 403 Asn Asn Pro Gln Ala Thr Arg Asp Ala Leu Asp Lys Asp Gly Trp Leu
 404 405 410 415
 407 His Thr Gly Asp Leu Gly Tyr Tyr Asp Glu Asp Arg Phe Ile Tyr Val
 408 420 425 430
 411 Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala
 412 435 440 445
 415 Pro Ala Glu Leu Glu Asn Leu Leu Leu Gln His Pro Asn Ile Ser Asp
 416 450 455 460
 419 Ala Gly Val Ile Gly Ile Pro Asp Glu Phe Ala Gly Gln Leu Pro Ser
 420 465 470 475 480
 423 Ala Cys Val Val Leu Glu Pro Gly Lys Thr Met Thr Glu Lys Glu Val
 424 485 490 495
 427 Gln Asp Tyr Ile Ala Glu Leu Val Thr Thr Thr Lys His Leu Arg Gly
 428 500 505 510
 431 Gly Val Val Phe Ile Asp Ser Ile Pro Lys Gly Pro Thr Gly Lys Leu
 432 515 520 525
 435 Met Arg Asn Glu Leu Arg Ala Ile Phe Ala Arg Glu Gln Ala Lys Ser
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 439 Lys Leu
 440 545
 443 <210> SEQ ID NO: 5
 444 <211> LENGTH: 1760
 445 <212> TYPE: DNA
 446 <213> ORGANISM: Phrixothrix Red Luciferase of US2002-0119542-A1
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 453 atcattataat aaatattcat atattactga cggaaataatc gatgcccata ccaatgaagt 180
 455 aatatcatat gctcaaataat ttgaaaccag ctgccgcttg gcagttagtc tagaaaaata 240
 457 tggcttggat cataacaatg ttgtggcaat atgcagtgaa aacaacatac actttttgg 300
 459 ccctttaatt gctgctttat accaaggaat accaatggca acatcaaatg atatgtacac 360

VERIFICATION SUMMARY DATE: 11/01/2006
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date